

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LASKY, LAURENCE A.
STACHELL, SCOTT E.
ROSEN, STEVEN D.
SINGER, MARK S.
YEDNOCK, TED A.

(ii) TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 20-Jul-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/513278

(B) FILING DATE: 10

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/059027

(B) FILING DATE: AUG-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/786149

(B) FILING DATE: 6-MAY1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/315015

(B) FILING DATE: 31-OCT-1991

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger R.

(B) REGISTRATION NUMBER: 33,055

(C) REFERENCE/DOCKET NUMBER: P0565D1C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-3216

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2259 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCCAGT GTGCTGGCTT CCTCACCTGC AGCACAGCAC ACTCCCTTTG 50
GCAAGGACCT GAGACCCTTG TGCTAAGTCA AGAGGCTCAA TGGGCTGCAG 100
AAGAACTAGA GAAGGACCAA GCAAAGCCAT GATATTTCCA TGGAAATGTC 150
AGAGCACCCA GAGGGACTTA TGGAACATCT TCAAGTTGTG GGGGTGGACA 200
ATGCTCTGTT GTGATTTTCT GGCACATCAT GGAACCTACT GCTGGACTTA 250
CCATTATTCT GAAAAACCCA TGAAGTGGCA AAGGGCTAGA AGATTCTGCC 300
GAGACAATTA CACAGATTTA GTTGCCATAC AAAACAAGGC GGAAATTGAG 350
TATCTGGAGA AGACTCTGCC CTTCAAGTCGT TCTTACTACT GGATAGGAAT 400
CCGGAAGATA GGAGGAATAT GGACGTGGGT GGGAACCAAC AAATCTCTCA 450
CTGAAGAAGC AGAGAACTGG GGAGATGGTG AGCCCAACAA CAAGAAGAAC 500
AAGGAGGACT GCGTGGAGAT CTATATCAAG AGAAACAAAG ATGCAGGCAA 550
ATGGAACGAT GACGCCTGCC ACAAACTAAA GGCAGCCCTC TGTTACACAG 600
CTTCTTGCCA GCCCTGGTCA TGCAGTGGCC ATGGAGAATG TGTAGAAATC 650
ATCAATAATC ACACCTGCAA CTGTGATGTG GGGTACTATG GGCCCCAGTG 700
TCAGCTTGTG ATTCAGTGTG AGCCTTTGGA GGCCCCAGAG CTGGGTACCA 750

TGGACTGTAC TCACCCCTTT GGAAACTTCA GCTTCAGCTC ACAGTGTGCC 800
 TTCAGCTGCT CTGAAGGAAC AACTTAACT GGGATTGAAG AAACCACCTG 850
 TGGACCATTT GGAAACTGGT CATCTCCAGA ACCAACCTGT CAAGTGATTC 900
 AGTGTGAGCC TCTATCAGCA CCAGATTTGG GGATCATGAA CTGTAGCCAT 950
 CCCCTGGCCA GCTTCAGCTT TACCTCTGCA TGTACCTTCA TCTGCTCAGA 1000
 AGGAACTGAG TTAATTGGGA AGAAGAAAAC CATTTGTGAA TCATCTGGAA 1050
 TCTGGTCAAA TCCTAGTCCA ATATGTCAAA AATTGGACAA AAGTTTCTCA 1100
 ATGATTAAGG AGGGTGATTA TAACCCCTC TTCATTCCAG TGGCAGTCAT 1150
 GGT TACTGCA TTCTCTGGGT TGGCATTAT CATTTGGCTG GCAAGGAGAT 1200
 TAAAAAAGG CAAGAAATCC AAGAGAAGTA TGAATGACCC ATATTAAATC 1250
 GCCCTTGGTG AAAGAAAATT CTTGGAATAC TAAAAATCAT GAGATCCTTT 1300
 AAATCCTTCC ATGAAACGTT TTGTGTGGTG GCACCTCCTA CGTCAAACAT 1350
 GAAGTGTGTT CCTTCAGTGC ATCTGGGAAG ATTTCTACCC GACCAACAGT 1400
 TCCTTCAGCT TCCATTTTCG CCCTCATTTA TCCCTCAACC CCCAGCCCAC 1450
 AGGTGTTTAT ACAGCTCAGC TTTTGTCTT TTCTGAGGAG AAACAAATAA 1500
 GACCATAAGG GAAAGGATTC ATGTGGAATA TAAAGATGGC TGACTTTGCT 1550

CTTTCTTGAC TCTTGTTTTT AGTTTCAATT CAGTGCTGTA CTTGATGACA 1600
 GACACTTCTA AATGAAGTGC AAATTTGATA CATATGTGAA TATGGACTCA 1650
 GTTTTCTTGC AGATCAAATT TCACGTCGTC TTCTGTATAC TGTGGAGGTA 1700
 CACTCTTATA GAAAGTTCAA AAAGTCTACG CTCTCCTTTC TTTCTAACTC 1750
 CAGTGAAGTA ATGGGGTCCT GCTCAAGTTG AAAGAGTCCT ATTTGCACTG 1800
 TAGCCTCGCC GTCTGTGAAT TGGACCATCC TATTTAACTG GCTTCAGGCC 1850
 TCCCCACCTT CTTCAGCCAC CTCTCTTTTT CAGTTGGCTG ACTTCCACAC 1900
 CTAGCATCTC ATGAGTGCCA AGCAAAGGA GAGAAGAGAG AAATAGCCTG 1950
 CGCGGTTTTT TAGTTTGGGG GTTTTGCTGT TTCCTTTTAT GAGACCCATT 2000
 CCTATTTCTT ATAGTCAATG TTTCTTTTAT CACGATATTA TTAGTAAGAA 2050
 AACATCACTG AAATGCTAGC TGCAAGTGAC ATCTCTTTGA TGTCATATGG 2100
 AAGAGTTAAA ACAGGTGGAG AAATTCCTTG ATTCACAATG AAATGCTCTC 2150
 CTTTCCCCTG CCCCAGAAC TTTTATCCAC TTACCTAGAT TCTACATATT 2200
 CTTTAAATTT CATCTCAGGC CTCCCTCAAC CCCACGGGGC CGCCAGCACA 2250
 CTGGAATTC 2259

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ile Phe Pro Trp Lys Cys Gln Ser Thr Gln Arg Asp Leu Trp
1 5 10 15

Asn Ile Phe Lys Leu Trp Gly Trp Thr Met Leu Cys Cys Asp Phe
20 25 30

Leu Ala His His Gly Thr Tyr Cys Trp Thr Tyr His Tyr Ser Glu
35 40 45

Lys Pro Met Asn Trp Gln Arg Ala Arg Arg Phe Cys Arg Asp Asn
50 55 60

Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Ala Glu Ile Glu Tyr
65 70 75

Leu Glu Lys Thr Leu Pro Phe Ser Arg Ser Tyr Tyr Trp Ile Gly
80 85 90

Ile Arg Lys Ile Gly Gly Ile Trp Thr Trp Val Gly Thr Asn Lys
95 100 105

Ser Leu Thr Glu Glu Ala Glu Asn Trp Gly Asp Gly Glu Pro Asn
110 115 120

Asn Lys Lys Asn Lys Glu Asp Cys Val Glu Ile Tyr Ile Lys Arg

Thr Phe Ile Cys Ser Glu Gly Thr Glu Leu Ile Gly Lys Lys Lys
 290 295 300

Thr Ile Cys Glu Ser Ser Gly Ile Trp Ser Asn Pro Ser Pro Ile
 305 310 315

Cys Gln Lys Leu Asp Lys Ser Phe Ser Met Ile Lys Glu Gly Asp
 320 325 330

Tyr Asn Pro Leu Phe Ile Pro Val Ala Val Met Val Thr Ala Phe
 335 340 345

Ser Gly Leu Ala Phe Ile Ile Trp Leu Ala Arg Arg Leu Lys Lys
 350 355 360

Gly Lys Lys Ser Lys Arg Ser Met Asn Asp Pro Tyr
 365 370 372

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2214 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCTCGA GCTCGTCGAC CACGCCCTCC TTGTGCAAGA ACTCTGAGCC 50

CCAGGTGCAG GAGGCTGAGG CCTGCAGAGA GACTTGCAGA GAGACCCAGC 100

GAGTTGGGTA CCATGGACTG CATCCACCCC TTGGGAAACT TCAGCTTCCA 950
 GTCCAAGTGT GCTTTCAACT GTTCTGAGGG AAGAGAGCTA CTTGGGACTG 1000
 CAGAAACACA GTGTGGAGCA TCTGGAAACT GGTCATCTCC AGAGCCAATC 1050
 TGCCAAGAGA CAAACAGAAG TTTCTCAAAG ATCAAAGAAG GTGACTACAA 1100
 CCCCCTCTTC ATTCCTGTAG CCGTCATGGT CACCGCATTC TCGGGGCTGG 1150
 CATTTCTCAT TTGGCTGGCA AGGCGGTTAA AAAAAGGCAA GAAATCTCAA 1200
 GAAAGGATGG ATGATCCATA CTGATTCATC CTTTGTGAAA GGAAAGCCAT 1250
 GAAGTGCTAA AGACAAAACA TTGGAAAATA ACGTCAAGTC CTCCCGTGAA 1300
 GATTTTACAC GCAGGCATCT CCCACATTAG AGATGCAGTG TTTGCTCAAC 1350
 GAATCTGGAA GGATTTCTTC ATGACCAACA GCTCCTCCTA ATTTCCCCTC 1400
 GCTCATTCAT CCCATTAACC CTATCCCATA ATGTGTGTCT ATACAGAGTA 1450
 GTATTTTATC ATCTTTTCTG TGGAGGAACA AGCAAAAGTG TTAGTGTA 1500
 ATATAAAGAC AGCTGCTTTT ACTCTTTCCT AACTCTTGTT TCCTAGTTCA 1550
 ATTCAGCACA GAAGCTAATG CCAAACACAG TGAAAATATG ATCCATGAGT 1600
 AATTGGAAAC TCAGACTCCT TGCGCATAGT ACGTACCCTA TGTAACATCG 1650
 ACAAAAATCT TTCATTTCCA CCTCCAAAGA ACAGTGCTCT ATTCAAGTTG 1700

GGAAAGTCCT ACTTCCTCTG TAGACCCACT ATCTGTGAGT GACAGCCACT 1750
GTAGCTGTTC ACATTAACCT TCCCCATCTC CTTTTCCTAG GAGAATAATT 1800
CCACACACTG CACCCCATGA TGGCCACCAA ACATCAAAGA AGGGAAAATC 1850
TCCTGCATTG AGTTTTAGTT TTGAGTTTTC CCTTCTCTTT ATTAGATCTC 1900
TGATGGTTCC TTGAAGTCAG TGTTCCTGATG ATTATTAATA GTTAATGATA 1950
ACACAACCCA CTCTCTTGGA GCTGATGTTA TGAAGACAAC AGGTAGAAAA 2000
ATTCCTGGGC TCAGGCTGGA GTGACACCCT TTTCTTTCCC TAACATCTTC 2050
TACTCAGATA CCTAAATTTA AGATTCAGGA CAGCTGTCCC CAACTCTTAC 2100
CATGTCTTTT ATAACTTGCT CCTTAACTTG CCCAACCTGT AGGCTATCTC 2150
ATTTTCTCGC TTCACTCTGC AAGGTTTATA ACATGATGAA TTAAATACA 2200
AAAAAAAAAA AAAA 2214

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Phe Pro Trp Arg Cys Glu Gly Thr Tyr Trp Gly Ser Arg

1	5	10	15
Asn Ile Leu Lys Leu Trp Val Trp Thr Leu Leu Cys Cys Asp Phe	20	25	30
Leu Ile His His Gly Thr His Cys Trp Thr Tyr His Tyr Ser Glu	35	40	45
Lys Pro Met Asn Trp Glu Asn Ala Arg Lys Phe Cys Lys Gln Asn	50	55	60
Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Arg Glu Ile Glu Tyr	65	70	75
Leu Glu Asn Thr Leu Pro Lys Ser Pro Tyr Tyr Tyr Trp Ile Gly	80	85	90
Ile Arg Lys Ile Gly Lys Met Trp Thr Trp Val Gly Thr Asn Lys	95	100	105
Thr Leu Thr Lys Glu Ala Glu Asn Trp Gly Ala Gly Glu Pro Asn	110	115	120
Asn Lys Lys Ser Lys Glu Asp Cys Val Glu Ile Tyr Ile Lys Arg	125	130	135
Glu Arg Asp Ser Gly Lys Trp Asn Asp Asp Ala Cys His Lys Arg	140	145	150
Lys Ala Ala Leu Cys Tyr Thr Ala Ser Cys Gln Pro Gly Ser Cys	155	160	165

Asn	Gly	Arg	Gly	Glu	Cys	Val	Glu	Thr	Ile	Asn	Asn	His	Thr	Cys
				170					175					180

Ile	Cys	Asp	Ala	Gly	Tyr	Tyr	Gly	Pro	Gln	Cys	Gln	Tyr	Val	Val
				185					190					195

Gln	Cys	Glu	Pro	Leu	Glu	Ala	Pro	Glu	Leu	Gly	Thr	Met	Asp	Cys
				200					205					210

Ile	His	Pro	Leu	Gly	Asn	Phe	Ser	Phe	Gln	Ser	Lys	Cys	Ala	Phe
				215					220					225

Asn	Cys	Ser	Glu	Gly	Arg	Glu	Leu	Leu	Gly	Thr	Ala	Glu	Thr	Gln
				230					235					240

Cys	Gly	Ala	Ser	Gly	Asn	Trp	Ser	Ser	Pro	Glu	Pro	Ile	Cys	Gln
				245					250					255

Val	Val	Gln	Cys	Glu	Pro	Leu	Glu	Ala	Pro	Glu	Leu	Gly	Thr	Met
				260					265					270

Asp	Cys	Ile	His	Pro	Leu	Gly	Asn	Phe	Ser	Phe	Gln	Ser	Lys	Cys
				275					280					285

Ala	Phe	Asn	Cys	Ser	Glu	Gly	Arg	Glu	Leu	Leu	Gly	Thr	Ala	Glu
				290					295					300

Thr	Gln	Cys	Gly	Ala	Ser	Gly	Asn	Trp	Ser	Ser	Pro	Glu	Pro	Ile
				305					310					315

Cys	Gln	Glu	Thr	Asn	Arg	Ser	Phe	Ser	Lys	Ile	Lys	Glu	Gly	Asp
				320					325					330

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

73

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGAAGCCCA TGAATTGGGA GAATGC 26

GAAGAAGCCCA TGAATTGGGA GAATGC 26